INPUT SET: S27164.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                                    SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5     (i) APPLICANT: Lee, James
 6                    Wood, WIlliam I.
 7
 8    (ii) TITLE OF INVENTION: PF4A Receptors
 9
10   (iii) NUMBER OF SEQUENCES: 6
11
12    (iv) CORRESPONDENCE ADDRESS:
13         (A) ADDRESSEE: Genentech, Inc.
14         (B) STREET: 1 DNA Way
15         (C) CITY: South San Francisco
16         (D) STATE: California
17         (E) COUNTRY: USA
18         (F) ZIP: 94080
19
20     (v) COMPUTER READABLE FORM:
21         (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22         (B) COMPUTER: IBM PC compatible
23         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24         (D) SOFTWARE: WinPatin (Genentech)
25
26    (vi) CURRENT APPLICATION DATA:
27         (A) APPLICATION NUMBER:
28         (B) FILING DATE: 24-June-1998
29         (C) CLASSIFICATION:
30
31   (vii) PRIOR APPLICATION DATA:
32         (A) APPLICATION NUMBER: 08/701265
33         (B) FILING DATE: 22-AUG-1996
34
35   (vii) PRIOR APPLICATION DATA:
36         (A) APPLICATION NUMBER: 08/664228
37         (B) FILING DATE: 06-JUN-1996
38
39   (vii) PRIOR APPLICATION DATA:
40         (A) APPLICATION NUMBER: 08/076093
41         (B) FILING DATE: 11-JUN-1993
42
43   (vii) PRIOR APPLICATION DATA:
44         (A) APPLICATION NUMBER: 07/810782
45         (B) FILING DATE: 19-DEC-1991
46
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INPUT SET: S27164.raw

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47   (viii) ATTORNEY/AGENT INFORMATION:
48         (A) NAME: Love, Richard B.
49         (B) REGISTRATION NUMBER: 34,659
50         (C) REFERENCE/DOCKET NUMBER: P0706P2C2
51
52    (ix) TELECOMMUNICATION INFORMATION:
53         (A) TELEPHONE: 415/225-5530
54         (B) TELEFAX: 415/952-9881
55         (C) TELEX: 910/371-7168
56
57   (2) INFORMATION FOR SEQ ID NO:1:
58
59    (i) SEQUENCE CHARACTERISTICS:
60         (A) LENGTH: 1933 base pairs
61         (B) TYPE: Nucleic Acid
62         (C) STRANDEDNESS: Single
63         (D) TOPOLOGY: Linear
64
65    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67
68   CCTGGCCGGT GCTTCAGTTA GATCAAACCA TTGCTGAAAC TGAAGAGGAC 50
69
70   ATGTCAAATA TTACAGATCC ACAGATGTGG GATTTTGATG ATCTAAATTT 100
71
72   CACTGGCATG CCACCTGCAG ATGAAGATTA CAGCCCCTGT ATGCTAGAAA 150
73
74   CTGAGACACT CAACAAGTAT GTTGTGATCA TCGCCTATGC CCTAGTGTTC 200
75
76   CTGCTGAGCC TGCTGGGAAA CTCCCTGGTG ATGCTGGTCA TCTTATACAG 250
77
78   CAGGGTCGGC CGCTCCGTCA CTGATGTCTA CCTGCTGAAC CTGGCCTTGG 300
79
80   CCGACCTACT CTTTGCCCTG ACCTTGCCCA TCTGGGCCGC CTCCAAGGTG 350
81
82   AATGGCTGGA TTTTTGGCAC ATTCCTGTGC AAGGTGGTCT CACTCCTGAA 400
83
84   GGAAGTCAAC TTCTACAGTG GCATCCTGCT GTTGGCCTGC ATCAGTGTGG 450
85
86   ACCGTTACCT GGCCATTGTC CATGCCACAC GCACACTGAC CCAGAAGCGT 500
87
88   CACTTGGTCA AGTTTGTTTG TCTTGGCTGC TGGGGACTGT CTATGAATCT 550
89
90   GTCCCTGCCC TTCTTCCTTT TCCGCCAGGC TTACCATCCA AACAATTCCA 600
91
92   GTCCAGTTTG CTATGAGGTC CTGGGAAATG ACACAGCAAA ATGGCGGATG 650
93
94   GTGTTGCGGA TCCTGCCTCA CACCTTTGGC TTCATCGTGC CGCTGTTTGT 700
95
96   CATGCTGTTC TGCTATGGAT TCACCCTGCG TACACTGTTT AAGGCCCACA 750
97
98   TGGGGCAGAA GCACCGAGCC ATGAGGGTCA TCTTTGCTGT CGTCCTCATC 800
99
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INPUT SET: S27164.raw

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100    TTCCTGCTTT GCTGGCTGCC CTACAACCTG GTCCTGCTGG CAGACACCCT 850
101
102    CATGAGGACC CAGGTGATCC AGGAGACCTG TGAGCGCCGC AACAACATCG 900
103
104    GCCGGGCCCT GGATGCCACT GAGATTCTGG GATTTCTCCA TAGCTGCCTC 950
105
106    AACCCCATCA TCTACGCCTT CATCGGCCAA AATTTTCGCC ATGGATTCCT 1000
107
108    CAAGATCCTG GCTATGCATG GCCTGGTCAG CAAGGAGTTC TTGGCACGTC 1050
109
110    ATCGTGTTAC CTCCTACACT TCTTCGTCTG TCAATGTCTC TTCCAACCTC 1100
111
112    TGAAAACCAT CGATGAAGGA ATATCTCTTC TCAGAAGGAA AGAATAACCA 1150
113
114    ACACCCTGAG GTTGTGTGTG GAAGGTGATC TGGCTCTGGA CAGGCACTAT 1200
115
116    CTGGGTTTTG GGGGGACGCT ATAGGATGTG GGGAAGTTAG GAACTGGTGT 1250
117
118    CTTCAGGGGC CACACCAACC TTCTGAGGAG CTGTTGAGGT ACCTCCAAGG 1300
119
120    ACCGGCCTTT GCACCTCCAT GGAAACGAAG CACCATCATT CCCGTTGAAC 1350
121
122    GTCACATCTT TAACCCACTA ACTGGCTAAT TAGCATGGCC ACATCTGAGC 1400
123
124    CCCGAATCTG ACATTAGATG AGAGAACAGG GCTGAAGCTG TGTCCTCATG 1450
125
126    AGGGCTGGAT GCTCTCGTTG ACCCTCACAG GAGCATCTCC TCAACTCTGA 1500
127
128    GTGTTAAGCG TTGAGCCACC AAGCTGGTGG CTCTGTGTGC TCTGATCCGA 1550
129
130    GCTCAGGGGG GTGGTTTTCC CATCTCAGGT GTGTTGCAGT GTCTGCTGGA 1600
131
132    GACATTGAGG CAGGCACTGC CAAAACATCA ACCTGCCAGC TGGCCTTGTG 1650
133
134    AGGAGCTGGA AACACATGTT CCCCTTGGGG GTGGTGGATG AACAAAGAGA 1700
135
136    AAGAGGGTTT GGAAGCCAGA TCTATGCCAC AAGAACCCCC TTTACCCCCA 1750
137
138    TGACCAACAT CGCAGACACA TGTGCTGGCC ACCTGCTGAG CCCCAAGTGG 1800
139
140    AACGAGACAA GCAGCCCTTA GCCCTTCCCC TCTGCAGCTT CCAGGCTGGC 1850
141
142    GTGCAGCATC AGCATCCCTA GAAAGCCATG TGCAGCCACC AGTCCATTGG 1900
143
144    GCAGGCAGAT GTTCCTAATA AAGCTTCTGT TCC 1933
145
146    (2) INFORMATION FOR SEQ ID NO:2:
147
148        (i) SEQUENCE CHARACTERISTICS:
149            (A) LENGTH: 350 amino acids
150            (B) TYPE: Amino Acid
151            (D) TOPOLOGY: Linear
152
```

153   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
154
155   Met Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe Asp Asp Leu
156   1   5   10   15
157
158   Asn Phe Thr Gly Met Pro Pro Ala Asp Glu Asp Tyr Ser Pro Cys
159   20   25   30
160
161   Met Leu Glu Thr Glu Thr Leu Asn Lys Tyr Val Val Ile Ile Ala
162   35   40   45
163
164   Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val
165   50   55   60
166
167   Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp
168   65   70   75
169
170   Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu
171   80   85   90
172
173   Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe
174   95   100   105
175
176   Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn
177   110   115   120
178
179   Phe Tyr Ser Gly Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg
180   125   130   135
181
182   Tyr Leu Ala Ile Val His Ala Thr Arg Thr Leu Thr Gln Lys Arg
183   140   145   150
184
185   His Leu Val Lys Phe Val Cys Leu Gly Cys Trp Gly Leu Ser Met
186   155   160   165
187
188   Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg Gln Ala Tyr His Pro
189   170   175   180
190
191   Asn Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly Asn Asp Thr
192   185   190   195
193
194   Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His Thr Phe Gly
195   200   205   210
196
197   Phe Ile Val Pro Leu Phe Val Met Leu Phe Cys Tyr Gly Phe Thr
198   215   220   225
199
200   Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln Lys His Arg Ala
201   230   235   240
202
203   Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp
204   245   250   255
205

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```
206      Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr
207                      260             265                 270
208
209      Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg
210                      275             280                 285
211
212      Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu His Ser Cys Leu
213                      290             295                 300
214
215      Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn Phe Arg His Gly
216                      305             310                 315
217
218      Phe Leu Lys Ile Leu Ala Met His Gly Leu Val Ser Lys Glu Phe
219                      320             325                 330
220
221      Leu Ala Arg His Arg Val Thr Ser Tyr Thr Ser Ser Ser Val Asn
222                      335             340                 345
223
224      Val Ser Ser Asn Leu
225                      350
226
227      (2) INFORMATION FOR SEQ ID NO:3:
228
229         (i) SEQUENCE CHARACTERISTICS:
230             (A) LENGTH: 1737 base pairs
231             (B) TYPE: Nucleic Acid
232             (C) STRANDEDNESS: Single
233             (D) TOPOLOGY: Linear
234
235         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
236
237
238      GAATTCCAGT GTGCTGGCGG CGCGGCGCAA AGTGACGCCG AGGGCCTGAG 50
239
240      TGCTCCAGTA GCCACCGCAT CTGGAGAACC AGCGGTTACC ATGGAGGGGA 100
241
242      TCAGTATATA CACTTCAGAT AACTACACCG AGGAAATGGG CTCAGGGGAC 150
243
244      TATGACTCCA TGAAGGAACC CTGTTTCCGT GAAGAAAATG CTAATTTCAA 200
245
246      TAAAATCTTC CTGCCCACCA TCTACTCCAT CATCTTCTTA ACTGGCATTG 250
247
248      TGGGCAATGG ATTGGTCATC CTGGTCATGG GTTACCAGAA GAAACTGAGA 300
249
250      AGCATGACGG ACAAGTACAG GCTGCACCTG TCAGTGGCCG ACCTCCTCTT 350
251
252      TGTCATCACG CTTCCCTTCT GGGCAGTTGA TGCCGTGGCA AACTGGTACT 400
253
254      TTGGGAACTT CCTATGCAAG GCAGTCCATG TCATCTACAC AGTCAACCTC 450
255
256      TACAGCAGTG TCCTCATCCT GGCCTTCATC AGTCTGGACC GCTACCTGGC 500
257
258      CATCGTCCAC GCCACCAACA GTCAGAGGCC AAGGAAGCTG TTGGCTGAAA 550
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/104,063*

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Line	Error	Original Text